AMENDMENTS

In the specification

1) Please replace the paragraph beginning on page 9, line13, with the following rewritten paragraph:

Figure 21. Secondary structure and transmembrane prediction for 85P1B3. Panel A. The secondary structure of 85P1B3 protein was predicted using the HNN - Hierarchical Neural Network method (Guermeur, 1997, ~~http:// pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_nn.html~~ pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=m[sa_nn.html), accessed from the ExPasy molecular biology server (~~http://www.expasy.ch/tools/~~ www.expasy.ch/tools/). This method indicates the presence and location of alpha helices (h), extended strands (e), and random coils (c) from the primary protein sequence. The percent of the protein in a given secondary structure is also given. Panel B. Schematic representation of the probability of existence of transmembrane regions of 85P1B3 based on the TMpred algorithm of Hofmann and Stoffel which utilizes TMBASE (K. Hofmann, W. Stoffel. TMBASE - A database of membrane spanning protein segments Biol. Chem. Hoppe-Seyler 374:166, 1993). Stretches of amino acids approximately 17-33 amino acids in length with a value greater than 0 are potential transmembrane helices. This program indicates the presence of one helix in 85P1B3. Panel C. Schematic representation of the probability of the existence of transmembrane regions and the extracellular and intracellular orientation of 85P1B3 based on the algorithm of Sonnhammer, von Heijne, and Krogh (Erik, L.L., et al., A hidden Markov model for predicting transmembrane helices in protein sequences. In Proc. of Sixth Int. Conf. on Intelligent Systems for Molecular Biology, p 175-182 Ed J. Glasgow, et al., Menlo Park, CA: AAAI Press, 1998). This program indicates 85P1B3 to be an intracellular protein without transmembrane domains. These transmembrane prediction results are also summarized in Table XXV.

2) Please replace Example 3 beginning on page 79, line 28, with the following rewritten example:

Example 3: Chromosomal Localization

Chromosomal localization can implicate genes in disease pathogenesis. Several chromosome mapping approaches are available in the art, including fluorescent *in situ* hybridization (FISH), human/hamster radiation hybrid (RH) panels (Walter et al., 1994; Nature Genetics 7:22; Research Genetics, Huntsville Al), human-rodent somatic cell hybrid panels such as is available from the Coriell Institute (Camden, New Jersey), and genomic viewers utilizing BLAST homologies to sequenced and mapped genomic clones (NCBI, Bethesda, Maryland).

85P1B3 maps to chromosome 15q14, using 85P1B3 sequence and the NCBI BLAST tool: (~~http://www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs~~ www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs).

The chromosomal localization of 85P1B3 was also determined using the GeneBridge4 Human/Hamster radiation hybrid (RH) panel (Walter et al., 1994; Nature Genetics 7:22) (Research Genetics, Huntsville Al).

The following PCR primers were used:

85P1B3.1 5' catgggactctgcatcttaattcc 3'

85P1B3.2 5' caggttcaggctttattgctgtct 3'

The resulting 85P1B3 mapping vector for the 93 radiation hybrid panel DNAs (10010001010100010100000000000011010000001210110000101110010000101110001001010110 0110110110101), and the mapping program available at the internet address ~~http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl~~ www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl, localize the 85P1B3 gene to chromosome 15q13.2- q14.

Of note, chromosome 15q13.2- q14 is a region implicated in cancers (Tomlinson et al., Gastroenterology 1999 Apr; 116(4):789-95).

3) Please replace TABLE XXV on page 170 with the following table:

TABLE XXV: Protein Properties

	Bioinformatic Program	URL	Outcome
ORF	ORF Finder	http://www.ncbi.nlm.gov/gorf	13-702 (includes stop)
Protein Length			229 amino acids
Transmembrane region	TM Pred	http://www.ch.embnet.org/	one TM at aa 129-149
	HMMTop	http://www.enzim.hu/hmmtop/	one TM at aa 134-158
	Sosui	http://www.genome.ad.jp/SOSui/	indicates no TM, soluble protein
	TMHMM	http://www.cbs.dtu.dk/services/TMHMM	indicates no TM
Signal Peptide	Signal P	http://www.cbs.dtu.dk/services/SignalP/	indicates no signal
pI	pI/MW tool	http://www.expasy.ch/tools/	pI 7.02
Molecular weight	pI/MW tool	http://www.expasy.ch/tools/	24.69 kDa
Localization	PSORT	http://psort.nibb.ac.jp/	Cytoplasmic 65 % Mitochondrial 10%
	PSORT II	http://psort.nibb.ac.jp/	Mitochondrial 60.9% Cytoplamic 21.7%
Motifs	Pfam	http://www.sanger.ac.uk/Pfam/	no motif detected
	Prints	http://www.biochem.ucl.ac.uk/	no significant motif
	Blocks	http://www.blocks.fhcrc.org/	Soybean trypsin inhibitor protease family, Cytochrome c
	Prosite	http://www.genome.ad.jp/	Cytochrome c family, heme binding signature